

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 24, 2005, 05:43:39 ; Search time 201 Seconds

(without alignments) 2165.421 Million cell updates/sec

Title: US-09-778-963B-2

Perfect score: 1377

Sequence: 1 MMKTLUSGNCNTLUSPVAKNSV IKAKVUREGQARRERDKCTIQ 266

Scoring table: BLOSUM62

XGAPOP 10.0 , XGAPEXT 0.5
 YGAPOP 10.0 , YGAPEXT 0.5
 FGAPOP 6.0 , FGAPEXT 7.0
 DelOp 6.0 , DeLext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 100%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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 -O=cgn2_1/USPTO_spool/b/US0977893/runat_22042005_151741_2383/app_query.fasta_1.455
 -DB=issued_Patents_NA -PFTM=fastab -SUFFIX=na -MINMATCH=0
 -LOGPREFIX=0 -UNITS=8192 -START=1 -END=-1 -MATRIX=BLOSUM62 -TRANS=human40.odd
 -LIST=45 -DOCLIGN=200 -THR SCORE=PCT -THR MIN=0 -ALIGN=15
 -MODE=LOCAL -OUTFMT=pl0 -NORM=ext -HEASIZE=500 -MINLEN=0 -MAXLEN=2000000000
 -USER=US0977893 @CGN_1_1_69 @runat_22042005_151741_2383 -NCPU=6 -ICPU=3
 -NO MMAP -LARGEQUERY -NSIG SCORES=0 -WAIT -DEBLOCK=100 -LONGLOG
 -DEV TIMEOUT=10 -WARN TIMEOUT=10 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=5
 -FGAPEXT=7 -YGAPOPA=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA.*

1: /cgn2_6/ptodata/1/ina/5a_COMB.seq: *
 2: /cgn2_6/ptodata/1/ina/5b_COMB.seq: *
 3: /cgn2_6/ptodata/1/ina/6a_COMB.seq: *
 4: /cgn2_6/ptodata/1/ina/6b_COMB.seq: *
 5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq: *
 6: /cgn2_6/ptodata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

RESULT 1
 US-09-709-103-40
 ; Sequence 40, Application US/09709103
 ; Sequence 40, Application US/09709103
 ; Patent No. 673391
 ; GENERAL INFORMATION:
 ; APPLICANT: Cisnowski, Mary
 ; APPLICANT: Duzic, Emir
 ; TITLE OF INVENTION: AGS Proteins and Nucleic Acid Molecules and Uses Therefor
 ; FILE REFERENCE: 60388-A-PCT-US
 ; CURRENT APPLICATION NUMBER: US/09/709,103
 ; CURRENT FILING DATE: 2000-11-08
 ; NUMBER OF SEQ ID NOS: 73
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO: 40
 ; LENGTH: 837

ALIGNMENTS

Alignment Scores:
 Pred. No.: 3.49e-180 Length: 837
 Score: 1372.00 Matches: 265
 Percent Similarity: 99.62% Conservative: 0
 Best Local Similarity: 99.62% Mismatches: 1
 Query Match: 99.64% Indels: 0
 DB: 4 Gaps: 0

US-09-778-963B-2 (1-266) x US-09-709-103-40 (1-837)

QY 1 MetMetLysThrLeuSerSergLyAsnCysThrLeuSerValProAlaLysSerTerTyr 20
 Db 37 ATGATGAGAGCTTGTCCAGGGAACTGACGCTCTAGTGTGCCGCAAACCTCATAC 96

Result	No.	Score	Query	Match	Length	DB	ID	Description
1	1372	99.6	837	4	US-09-709-103-40	Sequence 40, Appli		
2	1372	99.6	837	4	US-09-439-110A-40	Sequence 40, Appli		
3	1372	99.6	837	4	US-09-949-016-5022	Sequence 5022, Appli		
4	911	66.2	9259	4	US-09-949-016-6764	Sequence 16764, Appli		
5	879	67.8	846	4	US-09-439-110A-1	Sequence 1, Appli		
6	879	67.8	846	4	US-09-439-110A-1	Sequence 1, Appli		
7	879	63.8	1740	4	US-09-709-103-45	Sequence 45, Appli		
8	879	63.8	1740	4	US-09-439-110A-45	Sequence 45, Appli		
9	879	63.8	1801	4	US-09-709-103-45	Sequence 3, Appli		
10	879	63.8	1801	4	US-09-439-110A-3	Sequence 3, Appli		
11	879	63.8	1841	3	US-09-053-374A-1	Sequence 1, Appli		
12	876.5	63.7	1689	3	US-09-053-374A-4	Sequence 4, Appli		

QY 207 GluTyrGlyAspAlaPheHisProArgProPheCysMetArgArgValLysGluMetAsp 226
 Db 7077 CAGTACGGGAGCCTTCACCCAGGCCCTTCAGTCATGCCCGCTCAAGAGATGAC 7136
 QY 227 AlaTyrGlyMetValSerProPheAlaArgProSerValLeuSerAspIleUlyTyr 246
 Db 7137 GCCTATGGATGGTCGCTCGCCCTGGCCCGCCAGCTAACGTCAGTCAAGTAC 7196
 QY 247 IleLysAlaLysValLeuArgGluGlyGlnAlaArgIleArgAspLysCysThrIle 266
 Db 7197 ATCAGGCGAAGGCTCTGGAGGAGCCAGGCCGAGGAGCAAGTGCACCATCG 7256
 RESULT 5
 US-09-778-103-1
 ; Sequence 1, Application US/09709103
 ; Patent No. 673991
 ; GENERAL INFORMATION:
 ; APPLICANT: Cismowski, Mary
 ; APPLICANT: Duzic, Emir
 ; TITLE OF INVENTION: AGS Proteins and Nucleic Acid Molecules and Uses Therefor
 ; FILE REFERENCE: 60388-A-PCT-US
 ; CURRENT APPLICATION NUMBER: US/09/778, 103
 ; NUMBER OF SEQ ID NOS: 73
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 846
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(843)
 ; OTHER INFORMATION:
 US-09-709-103-1
 Alignment Scores:
 Pred. No.: 9.22e-112
 Score: 879.00
 Percent Similarity: 77.70%
 Best Local Similarity: 61.87%
 Query Match: 63.83%
 DB: 4
 DB: 4
 US-09-778-963B-2 (1-266) x US-09-709-103-1 (1-846)
 QY 1 MetMetLysThrLeuSerSerGlyAsnCysThrLeuSerValProAlaLysAsnSerTyr 20
 Db 16 ATGATCAAGAAGATGNGCCGAGCACTCGGAGCTGAGTACCCGGCAAGAACCTGTAT 75
 QY 21 ArgMetValValLeuGlyAlaSerArgValGlyIleSerSerIleValSerArgPheLeu 40
 Db 76 CGCAGTGTCTCCCTGGCTCCAGGCGCAGACGCCATCGTGTGCGCTTCCTC 135
 QY 41 AsnGlyArgGlyPheGluAspGlyIleThrProThrIleGluAspHeHisArgIleVal 60
 Db 136 ACCGGCCGCTCAGAACGCCCTAACGCCATACCGCTTACCTCGAGGACTCCACCGCAAGTCTAC 195
 QY 61 AsnIleArgGlyAspMetArgIleLeuAspIleLeuAspThrSerGlyAsnHisProHe 80
 Db 196 TCCATCGCGCGGAGGTCTTACCAACTCTGAACTCTGACACGTCGCGCAACACCGGTC 255
 QY 81 ProAlaMetArgArgLeuSerIleLeuThrGlyAspValAlaPheLeuValPheSerLeu 100
 Db 256 CCCGCCATCGGGCCTCTTCATCCTACAGAGAGCTTCATCCGGTGTCTAGCTG 315
 QY 101 AspAsnArgGlyUserPheAspGluValLeuAspGlyLeuGlyIleLeuIleLeuIle 120
 Db 316 GACACCCGCGACTCTTGAGGGTGGAGCCTCAGGCCAGCTCTGACACCAAG 375
 QY 121 SerCysLeuIuLysIleThrIleGluValAlaIleIleIleLeuIleLeuIleLeuIle 140
 Db 376 TCTTGCCCTCAAGACACACCAAGGAGGACCTGGTGGAGCCTGGCTCATCTGCGCAAC 435
 RESULT 6
 US-09-139-410A-1
 ; Sequence 1, Application US/09439410A
 ; Patent No. 674682
 ; GENERAL INFORMATION:
 ; APPLICANT: Cismowski, Mary
 ; APPLICANT: Duzic, Emir
 ; TITLE OF INVENTION: AGS PROTEIN AND NUCLEIC ACID MOLECULES AND USES THEREOF
 ; FILE REFERENCE: 191960388-B
 ; CURRENT APPLICATION NUMBER: US/09/439, 410A
 ; NUMBER OF SEQ ID NOS: 118
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 846
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(843)
 ; OTHER INFORMATION:
 US-09-439-410A-1
 Alignment Scores:
 Pred. No.: 9.22e-112
 Score: 879.00
 Percent Similarity: 77.70%
 Best Local Similarity: 61.87%
 Query Match: 63.83%
 DB: 4
 DB: 4
 US-09-778-963B-2 (1-266) x US-09-439-410A-1 (1-846)
 QY 1 MetMetLysThrLeuSerSerGlyAsnCysThrLeuSerValProAlaLysAsnSerTyr 20
 Db 16 ATGATCAAGAAGATGNGCCGAGCACTCGGAGCTGAGTACCCGGCAAGAACCTGTAT 75
 QY 21 ArgMetValValLeuGlyAlaSerArgValGlyIleSerSerIleValSerArgPheLeu 40
 Db 76 CGATGGCATCTGGCTGGAGGAGCTGGGGCAAGAGGCCATCTGTCGCTTC 135
 QY 41 AsnGlyArgGlyPheGluAspGlyIleThrProThrIleGluAspHeHisArgIleVal 60
 Db 136 ACCGGCCGCTCAGAACGCCCTAACGCCATACCGCTTACCTCGAGGACTCCACCGCAAC 195

RESULT 10
US-09-439-410A-3
; Sequence 3, Application US/09439410A
; GENERAL INFORMATION:
; APPLICANT: Duzic, Emil
; PATENT NO. 6746852
; TITLE OF INVENTION: AGS PROTEIN AND NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: 191960388-B
; CURRENT APPLICATION NUMBER: US/09/439, 410A
; CURRENT FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1601
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: CDS
; NAME/KEY: CDS
; LOCATION: (154)..(996)
; OTHER INFORMATION:
; US-09-439-410A-3

Alignment Scores:
Pred. No.: 3.21e-111 Length: 1801
Score: 879.00 Matches: 172
Percent Similarity: 77.70% Conservative: 44
Best Local Similarity: 61.87% Mismatches: 46
Query Match: 63.83% Indels: 15
DB: 4 Gaps: 4

RESULT 11
US-09-053-374A-1
; Sequence 1, Application US/09053374A
; Patent No. 6462177
; GENERAL INFORMATION:
; APPLICANT: YEN, KWANG-MU
; TITLE OF INVENTION: MAMMALIAN BLOOD LOSS-INDUCED GENE, KD312
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: ONE AMGEN CENTER DRIVE
; CITY: THOUSAND OAKS
; STATE: CA
; COUNTRY: US
; ZIP: 91320

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-98/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: COOK, ROBERT R.
; REGISTRATION NUMBER: 31, 602
; REFERENCE/DOCKET NUMBER: A-514
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1841 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 255..1097

RESULT 12
121 SerCysLeuIysAsnIysThrLysGluAlaAlaGluLeuProMetValleCysGlyIysIys 140
; Db 469 GACACCGCAGCTCTCGAGAGTCGAGGAGTCAGCAGCTCTCGACACAG 528
; Qy 529 TCTTGCTCTGAGAGAACAAACGAGGAGAGTCGAGGAGTCGAGCCTGCTCGGGCAC 589
; Db 141 LysAsnAspHisIysGlyIysLeuCysArgGlnValProThrThrGluAlaGluLeuVal 160
; Qy 589 AAGGGTGCAGCGC---GACTCTACCGCGAGTCAGCAGCAGCTGGTG 645
; Db 161 SerGlyAsp---GluAsnSerAlaTyPheGluValSerAlaLysLysGlyAsnThrAsnVal 179
; Qy 646 GGCGAGACCCCGCAGGCGCTCGCCCTACTGGAGATCTCGGAGACAGCCTGCG 705
; Db 180 AspGluMetPheTyPheLeuPheSerMetAlaLysLeuProHISGluMetSerProAla 199
; Qy 706 GACCACTTCCCGCCTCTGCCTGCGAGCTGCTGAGATGAGCCAG 765
; Db 200 LeuIysAspIysLeuValGlyIysArgIysAlaAlaPheHisProArgPropheCysMet 219
; Qy 766 CGGACACAGAGCTGCTCGGGCGGGAGCGGGCGGGCGACCCGGGAGCGCC 879
; Db 220 AspGlyValLeuIysGluMet-----AspAla 227
; Qy 820 TTGGCATCGGCGACCTCTGGCGAGCCACGCTACAGGACCTATGTCATC 939
; Db 228 TyrGlyMetValSerProPheAlaLysArgProSerValIysSerAlaPheLeuVal 247
; Qy 880 TTGGCATCTGCGACCTCTGGCGAGCCACGCTACAGGACCTATGTCATC 919
; Db 248 LysAlaLysValLeuArgGluLysGlyIysAlaArgGluIysGlyAspLysCysThrIle 265
; Qy 940 CGCGAGAAAGCCACGCCGCCAGCCAGGCCAGGAGGCGCTGGCTCATC 933

RESULT 13
US-09-778-963B-2 (1-266) x US-09-410A-3 (1-1801)
; Sequence 1, Application US/09410A-3
; Patent No. 6746852
; GENERAL INFORMATION:
; APPLICANT: Cimrowski, Mary
; TITLE OF INVENTION: AGS PROTEIN AND NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: 191960388-B
; CURRENT APPLICATION NUMBER: US/09/439, 410A
; CURRENT FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1601
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: CDS
; NAME/KEY: CDS
; LOCATION: (154)..(996)
; OTHER INFORMATION:
; US-09-439-410A-3

Alignment Scores:
Pred. No.: 3.21e-111 Length: 1801
Score: 879.00 Matches: 172
Percent Similarity: 77.70% Conservative: 44
Best Local Similarity: 61.87% Mismatches: 46
Query Match: 63.83% Indels: 15
DB: 4 Gaps: 4

RESULT 14
US-09-053-374A-1
; Sequence 1, Application US/09053374A
; Patent No. 6462177
; GENERAL INFORMATION:
; APPLICANT: YEN, KWANG-MU
; TITLE OF INVENTION: MAMMALIAN BLOOD LOSS-INDUCED GENE, KD312
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: ONE AMGEN CENTER DRIVE
; CITY: THOUSAND OAKS
; STATE: CA
; COUNTRY: US
; ZIP: 91320

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-98/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: COOK, ROBERT R.
; REGISTRATION NUMBER: 31, 602
; REFERENCE/DOCKET NUMBER: A-514
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1841 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 255..1097

RESULT 15
101 AspAsnArgGluSerPheAspGluValLysArgLeuGlnIysGlnIleLeuGluValLys 120

US-09-053-374A-1

Alignment Scores:

Pred. No.: 3.33e-111

Score: 879.00

Percent Similarity: 77.70%

Best local Similarity: 61.87%

Query Match: 63.83%

Length:

1841

Matches:

172

Conservative:

44

Mis matches:

46

Indels:

16

Gaps:

4

US-09-778-963B-2 (1-266) x US-09-053-374A-1 (1-1841)

QY 1 MetMetIysThrLeuSerSerGlyAsnCysThrLeuSerValProAlaAsnSerTyr 20

Db 270 ATGATCAGAACATGTCGCCGAGCAGACTCGCTGAGCTGAGTATCCGCCAGAGCTAT 329

QY 21 ArgMetValValLeuGlyAlaSerGlyAsnValGlyLysSerSerLeuValSerArgPheLeu 40

Db 330 CGCATGGTCATCCTCGCTCTCCAAAGTGGAGAACGCCATGGTGCGCTTCCTC 389

QY 41 AsnGlyArgPheGluAspGlyLysSerGlyAsnValGlyLysSerSerLeuValSerArgPheLeu 40

Db 390 ACCGGCGCTTCGAGGACGCCAACGGCTTACAGGCCATGGAGCTCCACCGAAGTCTAC 449

QY 61 AsnIleArgGlyAspMetTyrGlyLeuAspIleLeuAspThrSerGlyAsnValPheLeu 80

Db 450 TCCATTCGGCGGAGGCTCTACAGCTGAGTCATGACCTCTGAGCTGGCGACCTCGTC 509

QY 81 ProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheLeuValPheSerIle 100

Db 510 CCCGCATGGCGGGCTCTCATCTCAGAGGAGCTTTCATCCTGCTGTCAGTGT 569

QY 101 AspAsnArgGluSerPheAspGluValLeuArgIleGlyAsnGlyAsnValPheLeu 120

Db 570 GACAACGCCACTCCCTCGAGGAGCTGAGGCCATGGCTCAGGAGATCTCTGACACCAAG 629

QY 121 SerCysLeuIysAsnLysThrGlyAsnValIleLeuLeuAspMetValIleCysGlyAsn 140

Db 630 TCTTGCTCTGAGAACAAACGAGGAGCTGGAGCTGCCCTGGGCTACCTGGGAC 689

QY 141 LysAsnAspIleGlyGluLeuCysGlyAsnValProIleThrGlyAlaGluLeuLeuVal 160

Db 690 AGGGTGACCC--GACTCTACGGAGGTGGACCGAGTCGGAGATCGAGCAGCTGGT 746

QY 161 SerGlyAsp---GluAsnSerSerIleTyrPheGluValSerAlaIysLeuAsnThrAsnVal 179

Db 747 GGCAGCGACCCCAAGCGCTCGCCCTACTCTGGAGATCTGGCCAGAACAAACAGCGCTG 806

QY 180 AspGluMetPheThrValLeuAspSerMetAlaIysLeuProIleGluMetSerProIle 199

Db 807 GACCGATGTCCTCCGCGCTCTGGCCAGGCCAGCCTGGAGATGACCCAGAC 866

QY 200 LeuIleSargLysIleSerValGlyItyArgIysAspAlaIlePheHisProArgProheCysMet 219

Db 867 CTGGACCGGAGGCTCTGGCTGAGCTACTCTGGAGCTGTCACAGAAG----GCCTG 920

QY 220 ArgArgValIleGlyAspMet-----AspAla 227

Db 921 CGGAGACAAAGCAGCTGGCGGGCGGCGACGGCGACCCGGGAGGCC 980

QY 228 TyrGlyMetValLeuArgGlyGlyAlaArgProSerValIleSerAspLeuIleAspTyrIle 247

Db 981 TTGGCATCTGGCTACCTCTCTATCTCAGAGAGCTTCTGTTAGCTA 1040

QY 248 LysAlaIleValLeuArgGlyGlyAlaArgProAspSerValIleAspAspLeuIleAspTyrIle 265

Db 1041 CGCGAGAGGCCAGCGCGGCCAGCCAGGACAGGACAGGCCCTCGTC 1094

RESULT 12

US-09-053-374A-4

Sequence 4, Application US/09053374A

Patent No. 6462177

; GENERAL INFORMATION:

APPLICANT: YEN, KWANG-MU

TITLE OF INVENTION: MAMMALIAN BLOOD LOSS-INDUCED GENE, KD312

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: AMGEN INC.

STREET: ONE AMGEN CENTER DRIVE

CITY: THOUSAND OAKS

STATE: CA

COUNTRY: US

ZIP: 91320

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #11.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/053,374A

FILING DATE: CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: COOK, ROBERT R.

REGISTRATION NUMBER: 31,602

REFERENCE/DOCKET NUMBER: A-514

SEQUENCE FOR SEQ ID NO: 4;

SEQUENCE CHARACTERISTICS:

LENGTH: 1689 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE: NAME/KEY: CDS

LOCATION: 132..971

US-09-053-374A-4

Alignment Scores:

Pred. No.: 6.41e-111

Score: 876.50

Percent Similarity: 77.98%

Best Local Similarity: 61.73%

Query Match: 63.65%

DB: 3

Gaps:

US-09-778-963B-2 (1-266) x US-09-053-374A-4 (1-1689)

QY 1 MetMetIysThrLeuSerSerGlyAsnCysThrLeuSerValProAlaAsnSerTyr 20

Db 207 ATGATCAGAACATGTCGCCAGCAGCTCTGAGTATCCGCCAGAGCTTC 266

QY 21 ArgMetValValLeuGlyAlaSerGlyAsnValGlyLysSerSerLeuValSerArgPheLeu 40

Db 267 ACGGGCCCTGGAGGAGCTTACCCCTACCTTGAGACTTCACCGAAGTTAC 326

QY 41 AsnGlyArgPheGluAspGlyLysSerGlyAsnValProIleLeuAspThrArgIleAsnValPhe 80

Db 327 TCGATCCGGCGGAGATCTTACCGAGTGTGACATCTGGGATCATCCGTT 386

QY 81 ProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheLeuValPheSerIle 100

Db 387 CCCGCATGGGGCGCTCTCTATCTCAGAGAGCTTCTGTTAGCTA 446

QY 101 AspAsnArgGluSerPheAspGluValLeuAspIleLeuAspAspLeuIleAspTyrIle 120

Db 447 GACACGGCGACTCTGGAGGCTGCAAGGCCACAGGAGCTAGACAC 506

QY 121 SerCysLeuIysAsnLysThrGlyAlaIleLeuLeuAspMetValIleCysGlyAsn 140

Db 507 TCTGTCTGAGAACAAACCAAGAGATGAGTGGAGCGGCGCTGGTACCTGGGAAAC 566

US-09-778-963B-2 (1-266) x US-09-053-374A-5 (1-3079)

Qy 141 LysSerAspHisGlyGlueuCySrgGlnValProThrThrGluAlaGluLeuVal 160
 Db 567 AAAGGGGACCGG--GACTCTACCGCGAAGTGAGCAGGGAGATGAGCAGCTGG 623
 Qy 161 SerGlyAsp--GluAsnSerAlaTyrPheGluValSerAlaValAlaLysAsnThrAsnVal 179
 Db 624 GGCAGTGACCCCTACGGTGTGCCGACTCGAGATCTCGCCAAAGAGATAGGGCTG 633
 Qy 180 AspGluMetPheTyrValLeuPheSerMetAlaLysLeuProHisGluMetSerProAla 199
 Db 684 GACCGATGATGTCGGCTGGCTTGGCATGGCAGACTGCTAGCGAGATGAGCCTGAC 743
 Qy 200 LeuHisGlyAlaSerValLeuGlnTyrGlyAspAlaPheHisProArgProPheCysMet 219
 Db 744 TTGACCGCAGAGTCTGCTGAGTCTGAGCTGAGCTGACAAAGAG---GCTCTG 797
 Qy 220 ArgGlyVallysGluMet-----AspAlaTyr 228
 Db 798 AGGACAGAAGCTCTGGCTGGCGAGGGAGCTGGGGAGCAGCAGAGATGGCTT 857
 Qy 229 GlyMetValSerProPheAlaArgProSerValAsnSerAspLeuLysTyrIleLeu 248
 Db 858 GGATCTTGCGCCCTTGCTGGCATGGAGCTAGGGTGTGACATGGCAGCTCATGATCATG 917
 Qy 249 AlaArgValLeuArgGluGlyGlnAlaArgGluArgAspLysCysThrIle 265
 Db 918 GAGAAACCGTGTAGCAGGCCAGCTAACGGACAGGAGCCTGCTGTCATC 968
 RESULT 13
 US-09-053-374A-6
 Sequence 6, Application US/09053374A
 Patent No. 6462177
 GENERAL INFORMATION:
 APPLICANT: YEN, KWANG-MU
 TITLE OF INVENTION: MAMMALIAN BLOOD LOSS-INDUCED GENE, KD312
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: AMGEN INC.
 STREET: ONE AMGEN CENTER DRIVE
 CITY: THOUSAND OAKS
 STATE: CA
 COUNTRY: US
 ZIP: 91320
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patient in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/053, 374A
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: COOK, ROBERT R.
 REGISTRATION NUMBER: 31,602
 REFERENCE/DOCKET NUMBER: A-514
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3079 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-09-053-374A-6
 Alignment Scores:
 Pred. No.: 1.28-102 Length: 3079
 Score: 820.00 Matches: 170
 percent Similarity: 66.56% Conservative: 45
 best Local Similarity: 52.63% Mismatches: 47
 Query Match: 59.55% Indels: 62
 DB: 3 Gaps: 5

Qy 1 MetMethylAspThrLeuSerSerGlyAsnCysThrLeuSerValProAlaLysAsnSerTyr 20
 Db 318 ATGATCAAGAGATGTGCCAAAGGACTCTGACTGAGATTCGGCTAC 377
 Qy 21 ArgMetValValGluValSerArgValGlyLysSerSerIleValSerArgPheLeu 40
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 Qy 88 ----- 88
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 Qy 89 -----LeuThrGlyAspValPhe 94
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 Qy 174 LysLysAsnThrAsnValLeuPheGluMetPheTyrValLeuPheSerMetAlaLysLeuPro 193
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 Qy 243 AspIleLysTyrIleLeuAlaLysValLeuArgGluGlyGlnAlaArgGluAspLys 262
 Db 1208 GACCTCATCATTCGTCGAGAAACCTGTCAGCAGCAGGCTAAGGACAAGGAGGCG 1267
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 US-09-053-374A-3

卷之三

Job time : 216 secs



GenCore version 5.1.6
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ON protein - nucleic search, using frame_plus_p2n model

Run on: April 24, 2005, 05:50:40 ; Search time 631 Seconds
 (without alignments) 2559.270 Million cell updates/sec

Title: US-09-778-963B-2

Perfect score: 1377

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 Delop 6.0 , Deletxt 7.0

Searched: 5633728 seqs, 3035525691 residues

Total number of hits satisfying chosen parameters: 11267455

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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2	1372	99.5	837	18 US-10-804-491-40	Sequence 40, Appl
3	1372	99.6	2832	10 US-09-918-715-174	Sequence 14, Appl
4	1372	99.6	2832	17 US-10-185-035-4	Sequence 174, Appl
5	1372	99.6	2832	18 US-10-474-754-174	Sequence 197, Appl
6	1372	99.6	2973	18 US-10-474-794-197	Sequence 197, Appl
7	1372	99.6	2973	18 US-10-474-794-197	Sequence 5134, Appl
8	1372	99.6	3058	18 US-10-723-860-5134	Sequence 292, Appl
9	1304	94.7	3020	18 US-10-474-794-292	Sequence 292, Appl
10	1304	94.7	3020	18 US-09-78-963A-3	Sequence 3, Appl
11	911	66.2	1600	17 US-10-185-033-11	Sequence 11, Appl
12	911	66.2	114771	18 US-10-723-860-458	Sequence 458, Appl
13	911	66.2	65.9	16 US-10-029-386-20951	Sequence 20951, Appl
14	902	65.9	846	18 US-10-804-491-1	Sequence 1, Appl
15	879	63.8	1740	18 US-10-804-491-45	Sequence 45, Appl
16	879	63.8	1744	14 US-10-197-666-87	Sequence 3, Appl
17	879	63.8	1801	18 US-10-804-491-3	Sequence 13, Appl
18	879	63.8	1801	18 US-10-804-491-3	Sequence 12, Appl
19	586	42.6	1021	17 US-10-321-039-13	Sequence 25123, A
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41	296	21.5	2297	18 US-10-322-81-73	Sequence 473, Appl
42	296	21.5	2340	15 US-10-06-698-1073	Sequence 1073, Appl
43	296	21.5	2624	15 US-10-034-817-186	Sequence 1186, Appl
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; Patent No. US20020115172A1					
; GENERAL INFORMATION:					
; APPLICANT: NEEDAM, Beena et al					
; TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS					
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE					
; PROTEINS, AND USES THEREOF					
; FILE REFERENCE: CLO112					
; CURRENT APPLICATION NUMBER: US/09-778, 963A					
; CURRENT FILING DATE: 2001-02-08					
; NUMBER OF SEQ ID NOS: 5					
; SOFTWARE: FastSeq For Windows Version 4.0					
; SEQ ID NO: 1					
; LENGTH: 3082					
; TYPE: DNA					
; ORGANISM: Homo sapiens					
US-09-778-963A-1					

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 Db 271 CGCATGGTGGTGTGGGCTGGCCAGCTGGCTGGCCAGAGCTCCATCGCTCGCTCT 330
 Qy 41 AsnGlyArgPheGluAspGlyInTrpProThrIleGluAspPheHisArgLysValTyr 60
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 Qy 61 AsnIleArgGlyAspMetTyrGlnLeuAspIleLeuAspPheSerGlyAsnHisPhe 80
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 Db 451 CCCGCCATGGCGCAGGCTGTCATCCCTCACAGGGATCTCTCATCTGGTTCAGCCCTG 510
 Qy 101 AspAspArgGluUserPheAspGluValLysArgLeuValLysGlnIleLeuGluValLys 120
 Db 511 GATAACGGGAGTCCTCTGAGTGGGCAAGGCCCTCAGAGCAGTCCTGGAGGTCAG 570
 Qy 121 SerCysLeuLysAsnLysThrLysGluIleAlaGluIleProMetValIleCysGlyAsn 140
 Db 571 TCTGCGCTGAAAGACAGACAGGAGGGCGCCGAGCTGCCATGTCATCTGTCAGCAAC 630
 Qy 141 LysAsnAspHisGlyGluLeuCysArgGlyInValProThrIleGluAspPheHisArgLysValTyr 60
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US-09-778-963B-2 (1-266) x US-10-804-491-40 (1-837)

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 Db 157 AATGCCGCTTGTGGAGGACGATCACCCACCATGAGGACTCCACCGTAAAGTAC 216
 Qy 61 AsnIleArgGlyAspMetTyrGlnLeuAspIleLeuAspPheSerGlyAsnHisPhe 80
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 Qy 201 HisArgLysIleSerValGlyInTrpGlyAspAlaPheHisProArgProPheCysMetArg 220
 Db 637 CTGCGAAGATCTCGTGCAGTGGACGCCCTCACCCAGGCCCTCTGAGCGC 696
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 CURRENT FILING DATE: 2004-03-19
 PRIOR APPLICATION NUMBER: US/09/779,103
 PRIOR FILING DATE: 2000-11-08
 NUMBER OF SEQ ID NOS: 73
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 TYPE: DNA
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 LOCATION: (1)..(834)
 OTHER INFORMATION:
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US-09-778-963B-2 (1-266) x US-10-804-491-40 (1-837)

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 Qy 41 AsnGlyArgPheGluAspGlyInTrpProThrIleGluAspPheHisArgLysValTyr 60
 Db 157 AATGCCGCTTGTGGAGGACGATCACCCACCATGAGGACTCCACCGTAAAGTAC 216
 Qy 61 AsnIleArgGlyAspMetTyrGlnLeuAspIleLeuAspPheSerGlyAsnHisPhe 80
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; Publication No. US2003017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; CANT: Bert Vogelstein
; APPLICANT: Kenneth Kitzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107_00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
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; US-09-918-715-174
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; BEST LOCAL SIMILARITY: 99.62%
; QUERY MATCH: 10
; DB: DB
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; DB 217 AACATCGCGCGGAGCTGACATCTCGATACCTCTCGAACACCCCTC 276
; QY 81 ProAlaMetArgGargLeuSerLeuThrLeuIleGluAspPheSerLeuLeuAlaPheSerLeu 100
; DB 277 CCCGCATGCGCAGGCTGTCATCCACGAGGGATCTCATCTGGTTGCGCTC 336
; QY 101 AspAsnArgGluSerPheAspLysValValGluLysGlnLeuLeuGluValVal 120
; DB 337 GATAACCGGGAGTCCTCGATGAGGTCAAGGCCCTCAGAGCAGRCCTGGAGTCAG 396
; QY 121 SerCysLeuLysAsnLysThrLysGluAlaAlaGluLeuProMetValLeuCysLysAla 140
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; QY 241 AsnSerAspLysThrLeuSerLysAlaLysValLeuArgLysGluLysAlaArgLysArg 260
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; QY 161 SerGlyAspGluAsnSerAlaLysPheGluValSerAlaLysLysBsnThrAsnVal 180
; DB 517 TCGGGAGCAGAAGCTGCCATTCGGAGGTGGCCAGAGAAGAACCAAGTGGAC 576
; QY 181 GluMetPheThrValLeuHeSerMetAlaLysLeuProHisGluMetSerProAlaLeu 200
; DB 577 GAGATGTTCTACGGCTCTCAGCTGCGCAAGCTGCCACAGATGAGCCCGCCCTG 636
; QY 201 HisArgLysLeuSerValGlnTyrGlyAlaPheHisProArgPheCysMetArg 220
; DB 697 CGCGTCAGGAGATGAGCCCTGCGCTGTCGCGCCGGCCAGCGTC 756
; DB 637 CATGCCAAGATCTCGTGCGTAGCTGGTGAAGCCCTCACCCAGGCCCTCTGATGCC 696
; QY 241 AsnSerAspLysThrLeuSerLysValLeuValLeuArgLysGluLysAlaArgLysArg 260
; DB 757 AACAGTGACCTCAAGTACATCAAGGCCAGGGTCCCTCGGGAAGGCCAGGCCGIGAGGG 816
; QY 261 AspLysThrLeuGln 266
; DB 817 GACAAGTGACCATCCAG 834
; DB 577 GAGATGTTCTACGGCTCTCAGCTGCGCAAGCTGCCACAGATGAGCCCGCCCTG 636
; QY 201 HisArgLysLeuSerValGlnTyrGlyAlaPheHisProArgPheCysMetArg 220
; DB 697 CGCGTCAGGAGATGAGCCCTGCGCTGTCGCGCCGGCCAGCGTC 756
; DB 637 CATGCCAAGATCTCGTGCGTAGCTGGTGAAGCCCTCACCCAGGCCCTCTGATGCC 696
; QY 221 ArgValLysGluMetAspAlaPheArgLysMetValSerProPheAlaArgProSerVal 240
; DB 697 CGCGTCAGGAGATGAGCCCTGCGCTGTCGCGCCGGCCAGCGTC 756
; DB 637 CATGCCAAGATCTCGTGCGTAGCTGGTGAAGCCCTCACCCAGGCCCTCTGATGCC 696
; QY 241 AsnSerAspLysThrLeuSerLysValLeuValLeuArgLysGluLysAlaArgLysArg 260
; DB 757 AACAGTGACCTCAAGTACATCAAGGCCAGGGTCCCTCGGGAAGGCCAGGCCGIGAGGG 816
; QY 261 AspLysThrLeuGln 266
; DB 817 GACAAGTGACCATCCAG 834
; DB 397 TCCGCGCTGAGAACAGACCAAGAGGCCGGAGCTGCCATCGTCATCTGTCAG 456
; QY 141 LysAsparAspGlyGluLeuCysArgGlnValProThrGluAlaGluLeuLeuVal 160
; DB 457 AAGACGACACGGCGAGCTGCGCCAGTGCACCCACCGAGCCAGCTGCTGGTC 516
; QY 161 SerGlyAspGluAsnSerAlaLysPheGluValSerAlaLysLysBsnThrAsnVal 180
; DB 517 TCGGGAGCAGAAGCTGCCATTCGGAGGTGGCCAGAGAAGAACCAAGTGGAC 576
; QY 181 GluMetPheThrValLeuHeSerMetAlaLysLeuProHisGluMetSerProAlaLeu 200
; DB 577 GAGATGTTCTACGGCTCTCAGCTGCGCAAGCTGCCACAGATGAGCCCGCCCTG 636
; QY 201 HisArgLysLeuSerValGlnTyrGlyAlaPheHisProArgPheCysMetArg 220
; DB 697 CGCGTCAGGAGATGAGCCCTGCGCTGTCGCGCCGGCCAGCGTC 756
; DB 637 CATGCCAAGATCTCGTGCGTAGCTGGTGAAGCCCTCACCCAGGCCCTCTGATGCC 696
; QY 221 ArgValLysGluMetAspAlaPheArgLysMetValSerProPheAlaArgProSerVal 240
; DB 697 CGCGTCAGGAGATGAGCCCTGCGCTGTCGCGCCGGCCAGCGTC 756
; DB 637 CATGCCAAGATCTCGTGCGTAGCTGGTGAAGCCCTCACCCAGGCCCTCTGATGCC 696
; QY 241 AsnSerAspLysThrLeuSerLysValLeuValLeuArgLysGluLysAlaArgLysArg 260
; DB 757 AACAGTGACCTCAAGTACATCAAGGCCAGGGTCCCTCGGGAAGGCCAGGCCGIGAGGG 816
; QY 261 AspLysThrLeuGln 266
; DB 817 GACAAGTGACCATCCAG 834
; DB 577 GAGATGTTCTACGGCTCTCAGCTGCGCAAGCTGCCACAGATGAGCCCGCCCTG 636
; QY 201 HisArgLysLeuSerValGlnTyrGlyAlaPheHisProArgPheCysMetArg 220
; DB 697 CGCGTCAGGAGATGAGCCCTGCGCTGTCGCGCCGGCCAGCGTC 756
; DB 637 CATGCCAAGATCTCGTGCGTAGCTGGTGAAGCCCTCACCCAGGCCCTCTGATGCC 696
; QY 221 ArgValLysGluMetAspAlaPheArgLysMetValSerProPheAlaArgProSerVal 240
; DB 697 CGCGTCAGGAGATGAGCCCTGCGCTGTCGCGCCGGCCAGCGTC 756
; DB 637 CATGCCAAGATCTCGTGCGTAGCTGGTGAAGCCCTCACCCAGGCCCTCTGATGCC 696
; QY 241 AsnSerAspLysThrLeuSerLysValLeuValLeuArgLysGluLysAlaArgLysArg 260
; DB 757 AACAGTGACCTCAAGTACATCAAGGCCAGGGTCCCTCGGGAAGGCCAGGCCGIGAGGG 816
; QY 261 AspLysThrLeuGln 266
; DB 817 GACAAGTGACCATCCAG 834
; DB 397 TCCGCGCTGAGAACAGACCAAGAGGCCGGAGCTGCCATCGTCATCTGTCAG 456
; QY 141 LysAsparAspGlyGluLeuCysArgGlnValProThrGluAlaGluLeuLeuVal 160
; DB 457 AAGACGACACGGCGAGCTGCGCCAGTGCACCCACCGAGCTGCTGGTC 516
; QY 161 SerGlyAspGluAsnSerAlaLysPheGluValSerAlaLysLysBsnThrAsnVal 180
; DB 517 TCGGGAGCAGAAGCTGCCATTCGGAGGTGGCCAGAGAAGAACCAAGTGGAC 576
; QY 181 GluMetPheThrValLeuHeSerMetAlaLysLeuProHisGluMetSerProAlaLeu 200
; DB 577 GAGATGTTCTACGGCTCTCAGCTGCGCAAGCTGCCACAGATGAGCCCGCCCTG 636
; QY 201 HisArgLysLeuSerValGlnTyrGlyAlaPheHisProArgPheCysMetArg 220
; DB 697 CGCGTCAGGAGATGAGCCCTGCGCTGTCGCGCCGGCCAGCGTC 756
; DB 637 CATGCCAAGATCTCGTGCGTAGCTGGTGAAGCCCTCACCCAGGCCCTCTGATGCC 696
; QY 221 ArgValLysGluMetAspAlaPheArgLysMetValSerProPheAlaArgProSerVal 240
; DB 697 CGCGTCAGGAGATGAGCCCTGCGCTGTCGCGCCGGCCAGCGTC 756
; DB 637 CATGCCAAGATCTCGTGCGTAGCTGGTGAAGCCCTCACCCAGGCCCTCTGATGCC 696
; QY 241 AsnSerAspLysThrLeuSerLysValLeuValLeuArgLysGluLysAlaArgLysArg 260
; DB 757 AACAGTGACCTCAAGTACATCAAGGCCAGGGTCCCTCGGGAAGGCCAGGCCGIGAGGG 816
; QY 261 AspLysThrLeuGln 266
; DB 817 GACAAGTGACCATCCAG 834
; DB 397 TCCGCGCTGAGAACAGACCAAGAGGCCGGAGCTGCCATCGTCATCTGTCAG 456
; QY 141 LysAsparAspGlyGluLeuCysArgGlnValProThrGluAlaGluLeuLeuVal 160
; DB 457 AAGACGACACGGCGAGCTGCGCCAGTGCACCCACCGAGCTGCTGGTC 516
; QY 161 SerGlyAspGluAsnSerAlaLysPheGluValSerAlaLysLysBsnThrAsnVal 180
; DB 517 TCGGGAGCAGAAGCTGCCATTCGGAGGTGGCCAGAGAAGAACCAAGTGGAC 576
; QY 181 GluMetPheThrValLeuHeSerMetAlaLysLeuProHisGluMetSerProAlaLeu 200
; DB 577 GAGATGTTCTACGGCTCTCAGCTGCGCAAGCTGCCACAGATGAGCCCGCCCTG 636
; QY 201 HisArgLysLeuSerValGlnTyrGlyAlaPheHisProArgPheCysMetArg 220
; DB 697 CGCGTCAGGAGATGAGCCCTGCGCTGTCGCGCCGGCCAGCGTC 756
; DB 637 CATGCCAAGATCTCGTGCGTAGCTGGTGAAGCCCTCACCCAGGCCCTCTGATGCC 696
; QY 221 ArgValLysGluMetAspAlaPheArgLysMetValSerProPheAlaArgProSerVal 240
; DB 697 CGCGTCAGGAGATGAGCCCTGCGCTGTCGCGCCGGCCAGCGTC 756
; DB 637 CATGCCAAGATCTCGTGCGTAGCTGGTGAAGCCCTCACCCAGGCCCTCTGATGCC 696
; QY 241 AsnSerAspLysThrLeuSerLysValLeuValLeuArgLysGluLysAlaArgLysArg 260
; DB 757 AACAGTGACCTCAAGTACATCAAGGCCAGGGTCCCTCGGGAAGGCCAGGCCGIGAGGG 816
; QY 261 AspLysThrLeuGln 266
; DB 817 GACAAGTGACCATCCAG 834

QY 61 AsnIleArgIlyAspMetTyrgInleusAspIleLeuAspThrSerIlyAsnHisProhe 80
 Db 217 ACATCCGGGCGACATGTCAGCTGCACTCTGGATACCTCTGCAACACCCCTC 276
 QY 81 ProAlaMetArgArgLeuSerIleLeuThrArgIlyAspValProLeuValPhsSerLeu 100
 Db 277 CCCGCATGGCAGGGCTGTCATCTCCTACAGGGATGCTTCATCTGGTTAGCCCTG 336
 QY 101 AspAspArgIlyAspLeuSerIleLeuThrArgIlyAspValProLeuValPhsSerLeu 100
 Db 337 GATAACCGGGAGAGCCTCTGGATGAGGTCAAGGCTTCAGAGCAATCCGGAG 395
 QY 121 SerCysIleuIlyAsnIlyThrIlyGluIleuAlaGluLeuProMetVallecySlyAsn 140
 Db 397 TCTGCGCTGAGAAGACAGAGCAAGGGCGGAGCTGCGCATGTCATCTGGCAAC 456
 QY 141 LysAsnAspHisIlyGluIleuCysArgInvalProThrIlyGluIleuGluVallys 160
 Db 457 ANGAACGACACAGGGCGAGCTGCCCCAAGTGCACCCACCGAGCCGGCTGAG 516
 QY 161 SerGlyAspIlyAsnSerIleIlyTyrPheIlyValSerAlaIlyAsnIlyAsn 180
 Db 517 TCGGGGAGAGAAGCTCGCTACTCTGAGCTGTCGGCCAGAGAACACACAGTGGAC 576
 QY 181 GluMetPheTyrvallLeuPheSerMetAlaIlyLeuProHisGluMetSerProAlaLeu 200
 Db 577 GAGATGTTCTACGTGCTCTCAGATGCGCAAGCTGCGCCACAGAGATGAGCCCGCCCG 636
 QY 201 HisArgLysIleSerValIlyTyrGlyAspValProLeuValPhsSerIleLeuVal 220
 Db 637 CATGCGAAGACTCCCGTGCAGCTGACGGCTTCCACCCAGCCCTCTGATGCGC 696
 QY 221 ArgValIlyGluMetAspAlaIlyTyrGlyMetValSerProPheIaArgArgProSerVal 240
 Db 697 CGCGTCAGAGAGATGGACGCCATGCTCTGCGCCCTCGCCCGGCCAGCGCTC 756
 QY 241 AsnSerAspLeuIlyTyrIlyLysAlaValLeuArgIlyGlyIleuArgIlyGluIleuGlu 260
 Db 757 AACAGTGACTCTCAAGTCATCAAGGCCAAGTCCTCTGGAGAAGGCCAGGCCGAGG 816
 QY 261 AspLysCysThrIleIgln 266
 Db 817 GACAAGTGCAACCATCG 834

RESULT 5
 US-10-474-794-174
 ; Sequence 174. Application US/10474794
 ; Publication No. US2002013793A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Carson-Walter, Eleanor
 ; ST. CROIX, Brad
 ; APPLICANT: Vogelstein, Bert
 ; APPLICANT: Kinzler, Kenneth
 ; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
 FILE REFERENCE: 1107.00179
 CURRENT APPLICATION NUMBER: US/10474,794
 CURRENT FILING DATE: 2003-10-14
 PRIOR APPLICATION NUMBER: 60/282,850
 PRIOR FILING DATE: 2001-04-11
 PRIOR APPLICATION NUMBER: 60/308,829
 PRIOR FILING DATE: 2001-08-01
 NUMBER OF SEQ ID NOS: 359
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 174
 LENGTH: 2832
 TYPE: DNA
 ORGANISM: Homo sapiens

Alignment Scores:
 Pred. No.: 1.23e-167 Length: 2832
 Score: 132.00 Matches: 265
 Percent Similarity: 99.52% Conservative: 0

Best Local Similarity: 99.62% Mismatches: 1
 Query Match: 99.64% Index: 0
 DB: 18 Gaps: 0

US-09-778-963B-2 (1-266) x US-10-474-794-174 (1-2832)

QY 1 MetMetIlyThrIleuSerSergIlyAspCysThrLeuSerValProAlaValSerTyr 20
 Db 37 ATGATGAAAGCTTGTGCGCGGAGCTGAGCTGCTGAGCTGCGCCGGCAAAACTCATAC 96
 QY 21 ArgMetValValLeuIlyAsnSerArgValGlyIlySerSerIleValSerArgPhsLeu 40
 Db 97 CGCATGTTGTTGCTGGTGGCTCTCGTGTGCGCCGGCAAAACTCATAC 156
 QY 41 AspGlyArgPheIlyGluIlyGlyIlyTyrIlyProThrIlyGluAspPheliSarglyValTyr 60
 Db 157 AATGGCCCTTGAGGAGCAGCAGACACACACTGGAC 216
 QY 61 AsnIleArgIlyAspMetTyrgInleuAspIleLeuAspThrSerIlyAsnHisProhe 80
 Db 217 ACATCCGGGCGACATGTCAGCTGCACTCTGGATACCTCTGCAACACCCCTC 276
 QY 81 ProAlaMetArgArgLeuSerIleLeuThrArgIlyAspValProLeuValPhsSerLeu 100
 Db 277 CCCGCATGGCAGCTGTCATCTCCTACAGGGATGCTTCATCTGGTTAGCCCTG 336
 QY 101 AspAspArgIlyAspLeuSerIleLeuThrArgIlyAsnIlyAsnIlyAsn 180
 Db 337 GATPACCGGAGACTCTCTGATGAGGTCAAGGCTTCAGAGCAATCCGGACTTCCACCGTAAAGTAC 216
 QY 121 SerCysIleuIlyAsnIlyThrIlyGluIleuAlaGluLeuProMetVallecySlyAsn 140
 Db 397 TCTGCGCTGAGAAGACATGTCAGCTGACCTGAGCTGCGCATGTCATCTGGCAAC 456
 QY 141 LysAsnAspHisIlyGluIleuCysArgInvalProThrIlyGluIleuGluVallys 160
 Db 457 ANGAACGACACAGGGCGAGCTGCCCCAAGTGCACCCACCGAGCCGGCTGAG 516
 QY 161 SerGlyAspIlyAsnSerIleIlyTyrPheIlyValSerAlaIlyAsnIlyAsn 180
 Db 517 TCGGGGAGAGAAGCTCGCTACTCTGAGCTGTCGGCCAGAGAACACACAGTGGAC 576
 QY 181 GluMetPheTyrvallLeuPheSerMetAlaIlyLeuProHisGluMetSerProAlaLeu 200
 Db 577 GAGATGTTCTACGTGCTCTCAGATGCGCAAGCTGCGCCACAGAGATGAGCCCGCC 636
 QY 201 HisArgLysIleSerValIlyTyrGlyAspValProLeuValPhsSerIleLeuVal 220
 Db 637 CATGCGAAGACTCCCGTGCAGCTGACGGCTTCCACCCAGCCCTCTGATGCGC 696
 QY 221 ArgValIlyGluMetAspAlaIlyTyrGlyMetValSerProPheIaArgArgProSerVal 240
 Db 697 CGCGTCAGAGAGATGGACGCCATGCTCTGCGCCCTCGCCCGGCCAGCGCTC 756
 QY 241 AsnSerAspLeuIlyTyrIlyLysAlaValLeuArgIlyGlyIleuArgIlyGluIleuGlu 260
 Db 757 AACAGTGACTCTCAAGTCATCAAGGCCAAGTCCTCTGGAGAAGGCCAGGCCGAGG 816
 QY 261 AspLysCysThrIleIgln 266
 Db 817 GACAAGTGCAACCATCG 834

RESULT 6
 US-09-918-715-197
 ; Sequence 197. Application US/09918715
 ; Publication No. US2002017157A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brad St. Croix
 ; APPLICANT: Bert Vogelstein
 ; APPLICANT: Kenneth Kinzler
 ; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
 FILE REFERENCE: 1107.00134
 CURRENT APPLICATION NUMBER: US/09/918,715

CURRENT FILING DATE: 2001-08-01
; PRIORITY APPLICATION NUMBER: 60/222,599
; PRIORITY FILING DATE: 2000-08-02
; PRIORITY APPLICATION NUMBER: 60/224,360
; PRIORITY FILING DATE: 2000-08-11
; PRIORITY APPLICATION NUMBER: 60/282,850
; NUMBER OF SEQ ID NOS: 358
; PRIORITY FILING DATE: 2000-04-11
; SEQ ID NO: 197
; LENGTH: 2973
; TYPE: DNA
; ORGANISM: Homo sapiens

Alignment Scores:
Pred. No.: 1.32e-167 Length: 2973
Score: 1372.00 Matches: 265
Percent Similarity: 99.62% Conservative: 0
Best Local Similarity: 99.62% Mismatches: 1
Query Match: 99.64% Indels: 0
DB: 10 Gaps: 0

US-09-778-963B-2 (1-266) x US-09-918-715-197 (1-2973)

Qy 1 MetMetLysThrLeuSerSerGlyAlaCysThrLeuSerValProAlaLysAsnSerTyr 20
Db 208 ATGATGAGACTTGTGCAACGGGAACTGCAAGCTGAGCTCAGTGTGCCGCCAAACATC 267

Qy 21 ArgMetValAlaLeuGlyAlaSerArgValGlyLysSerSerLeuValSerArgPheLeu 40
Db 268 CGCAGCTGTGCTGCTGGCTGCTGGCTGGCAAGAGCTTCCATCTGTGTCTGCCTTC 327

Qy 41 AsnGlyArgPheGluAspGlyLysThrProThrIleGluAspPheHisArgLysValTyr 60
Db 328 AATGCCGCTTGTGCAACGGGAACTGCAAGCTGAGCTCAGTGTGCCAACCCCTTC 387

Qy 61 AsnLysArgGlyAspMetTyrGlnLeuAspIleLeuAspThrSerGlyAlaAsnHisProhe 80
Db 388 AACATCGCCGCGGACATGTACAGTCAGTCGACATCTGGATACCTCTGGCAACCCCTTC 447

Qy 81 ProLysMetArgArgLeuSerIleLeuThrGlyAspValPheIleLeuValPheSerLeu 100
Db 448 CCCGCCATGCGCAGCTGTCTCATCTGGTTCATCTGGTTCAGCCTG 507

Qy 101 AspAsnArgGluSerPheAspIleLeuAspIleLeuAspThrSerGlyAlaAsnHisProhe 120

Db 508 GATAACGGGAACTCTCTGAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAG 567

Qy 121 SerCysLeuLysAsnSerIleLeuAspIleLeuAspIleLeuAspThrSerGlyAlaAsn 140

Db 568 TCTGCTCTGAGAGCAGACGAGGAGGCGGGAGCTGCCATGTCTCATCTGGCAAC 627

Qy 141 LysAsnAspIsglLysLeuCysArgGlyAlaProThrIleGluAlaGluLeuLeuVal 160

Db 628 AAGAACGACCAACGGCGAGCTGGCCACCCGGAGCCGGAGCTGG 687

Qy 161 SerGlyAspGluAsnSerIleLeuAspIleLeuAspIleLeuAspThrSerGlyAlaAsn 180

Db 688 TGGGGGACCGGAACTCGCTACTCGAGCTGCGCTGGCCAGAGAACCCAACTGGAC 747

Qy 181 GluMetPheTyrValLeuPheSerMetAlaIleLeuProIleGluMetSerProIleLeu 200

Db 748 GAGAGTCTCTGCTCTCTGAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAG 807

Qy 201 HisArgLysGluMetAspIleLeuSerValGlyAspValSerProIleLeuAspProIleCysMetArg 220

Db 808 CATGCCAAGATCTCTGGCTGAGCTGACCTACCCAGGCCCTCTGCTGAGCTGAGCTGAGC 867

Qy 221 ArgValLysGluMetAspIleLeuSerValGlyAspValSerProIleLeuAspProIleLeuAspSerIle 240

Db 868 CGGTCGAAGGAGATGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGC 927

RESULT 7
US-10-474-794-197
; Sequence 197, Application US/10474794
; Publication No. US20040213793A1
; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.0019
; CURRENT APPLICATION NUMBER: US/10/474,794
; CURRENT FILING DATE: 2003-10-14
; PRIORITY APPLICATION NUMBER: 60/282,850
; PRIORITY FILING DATE: 2001-04-11
; PRIORITY APPLICATION NUMBER: 60/308,829
; PRIORITY FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 197
; LENGTH: 2973
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-474-794-197

Alignment Scores:
Pred. No.: 1.32e-167 Length: 2973
Score: 1372.00 Matches: 265
Percent Similarity: 99.62% Conservative: 0
Best Local Similarity: 99.62% Mismatches: 1
Query Match: 99.64% Indels: 0
DB: 18 Gaps: 0

US-09-778-963B-2 (1-266) x US-10-474-794-197 (1-2973)

Qy 1 MetMetLysThrLeuSerSerGlyAlaCysThrLeuSerValProAlaLysAsnSerTyr 20
Db 208 ATGATGAGACTTGTGCAACGGGAACTGCAAGCTGAGCTCAGTGTGCCGCCAAACATC 267

Qy 21 ArgMetValAlaLeuGlyAlaSerArgValGlyLysSerSerLeuValSerArgPheLeu 40
Db 268 CGCAGCTGTGCTGCTGGCTGCTGGCTGGCAACCCCTTC 327

Qy 41 AsnGlyArgPheGluAspGlyLysThrProThrIleGluAspPheHisArgLysValTyr 60
Db 328 AATGCCGCTTGTGCAACGGGAACTGCAAGCTGAGCTCAGTGTGCCAACCCCTTC 387

Qy 61 AsnLysArgGlyAspMetTyrGlnLeuAspIleLeuAspThrSerGlyAlaAsnHisProhe 80
Db 388 AACATCGGGCGGAGCTGAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAG 447

Qy 81 ProLysMetArgArgLeuSerIleLeuThrGlyAspValPheIleLeuValPheSerLeu 100
Db 448 CCCGCCATGCGCAGCTGTCTCATCTGGTTCATCTGGTTCAGCCTG 507

Qy 101 AspAsnArgGluSerPheAspGluAlaLysAspGlyLysGlnLeuLeuGluValLys 120

Db 508 GATAACGGGAACTCTCTGAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAG 567

Qy 121 SerCysLeuLysAsnSerIleLeuAlaGluLeuProMetValLeuCysGlyAlaAsn 140

Db 568 TCTGCTCTGAGAGCAGACGAGGAGGCGGGAGCTGCCATGGCATCTGGCAAC 627

Qy 141 LysAsnAspIsglLysLeuCysArgGlyAlaProThrIleGluAlaGluLeuLeuVal 160

Db 1096 AACAGTGTACCTCAAGGCCAAGGTCCTACGGGAGGGCCAGGGAGAGAGG 1155
 Qy 261 AspLyCysThrIleGln 266
 Db 1156 GAGAGTGTAGCATCCAG 1173

RESULT 11
 US-09-778-963A-3
 Sequence 3, Application US/0978963A
 Patent No. US20020115172A1
 GENERAL INFORMATION:
 ; APPLICANT: NEELAM, Beena et al
 ; TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
 ; TITTLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
 ; FILE REFERENCE: CI001112
 ; CURRENT APPLICATION NUMBER: US/09/778, 963A
 ; CURRENT FILING DATE: 2001-02-08
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 11221
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-778-963A-3

Alignment Scores:
 Pred. No.: 1.56e-106
 Score: 911.00
 Percent Similarity: 98.33%
 Best Local Similarity: 97.78%
 Query Match: 66.16%
 Db: 99
 ; US-09-778-963B-2 (1-1221) (1-11221)

Qy 87 SerIleLeuThrGlyAspValPheIleLeuPheSerLeuAspAsnArgLysPhe 106
 Db 7681 TCTCCTCCCTGAGGGATGTCCTTCATCTCTGTCAGCTTGTGAAACCGGGACTTC 7740

Qy 107 AspGluValLysArgLeuGlyAsnIleLeuGluValLysSerCysIleLeuAsnLys 126
 Db 7741 GATGAGGTCAAGGGCTTCAGAAGCAGATCTGGAGTCAGTCCTGGCTGAAGAACAG 7800

Qy 127 ThrLyGluIalaAlaGluLeuProMetValIleCysGlyAlaLysIleAsnAsp 146
 Db 7801 ACCAAGGAGCCGGCGAGCAGCCATGGTACATCTGGCAACAGACCAAGGGAG 7860

Qy 147 LeuCysBargIValProThrThrGluIalaGluLeuLeuValSerGlyAspGluAsnSer 166
 Db 7861 CTGAGCCGGAGGAGCAGCCACACCGAGCCAGCTGCTGTCGGGCCAGAGAAGCTGC 7920

Qy 167 AlaTyrPheGluValSerAlaLysAsnThrAsnValAspGluMetPheTyrValLeu 186
 Db 7921 ACCCTCTCAGGTTGGCAAGAGAACACCAAGCTGAGATGTTCTAGTGTCTAGTC 7980

Qy 187 PheserMetAlaLysLeuProIleGlyAsnSerProAlaLeuHisArgLysIleSerVal 206
 Db 7981 TTCAAGCATGCCAACGCTGCCACAGCAGATGCCAGCCGCGCCCTGATGCCAGAGCTCG 8040

Qy 207 GluTyrGlyAspAlaPheHisProArgProHeCysMetArgArgValLysGluMetAsp 226
 Db 8041 CAGTACGGTACGCCCTCCACCCAGGCCCTCTGCACTGCCCGCTGAGAGATGAC 8100

Qy 227 AlaTyrGlyMetValSerProHeAlaArgProSerValAsnSerAspLeuLysTyr 246
 Db 8101 GGCATATGGCTTGGCTCCCTGCCGCCAGGCTCACAGTCAGCTCAAGTAC 8160

Qy 247 IleLysAlaLysValLeuArgGluLysGlnAlaArgGluLysAspLysCysThrIleGln 266
 Db 8161 ATCAGGCCAAGGCTCTGGGAAGGCCAGGCCGTTGAGGACAAGTGACCATCCAG 8220

RESULT 12
 ; Sequence 11, Application US/10185035
 ; Publication No. US20040005706A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brett P. Monia
 ; APPLICANT: Kenneth W. Dobie
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF DEXRAS1 EXPRESSION
 ; FILE REFERENCE: RIS-0377
 ; CURRENT APPLICATION NUMBER: US/10/185, 035
 ; CURRENT FILING DATE: 2002-06-28
 ; NUMBER OF SEQ ID NOS: 135
 ; SEQ ID NO 11
 ; LENGTH: 16000
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-185-035-11

Alignment Scores:
 Pred. No.: 2.73e-106
 Score: 911.00
 Percent Similarity: 98.33%
 Best Local Similarity: 97.78%
 Query Match: 66.16%
 Db: 17
 ; US-09-778-963B-2 (1-366) x US-10-185-035-11 (1-16000)

Qy 87 SerIleLeuThrGlyAspValPheIleLeuPheSerLeuAspAsnArgLysPhe 106
 Db 11913 TCTCCTCCCTGAGGGATGTCCTTCATCTCTGTCAGCTTGTGAAACCGGGACTTC 11972

Qy 107 AspGluValLysArgLeuGlyAsnIleLeuGluValLysSerCysIleLeuAsnLys 126
 Db 11973 GATGAGGTCAAGGGCTTCAGAAGCAGATCTGGAGTCAGTCCTGGCTGAAGAACAG 12032

Qy 127 ThrLyGluIalaAlaGluLeuProMetValIleCysGlyAlaLysIleAsnAsp 146
 Db 12033 ACCAAGGAGCCGGAGCTGCCATGTCATCTGGCAACAGACCAAGGGAG 12092

Qy 147 LeuCysBargIValProThrThrGluIalaGluLeuLeuValSerGlyAspGluAsnSer 166
 Db 12093 CTGAGCCGGAGCTGCCATGGCCAGAGAACCAAGGGCCAGCTGCTGGCTGGAGAAGACTGC 12152

Qy 167 AlaTyrPheGluValSerAlaLysAsnThrAsnValAspGluMetPheTyrValLeu 186
 Db 12153 GCCTACTCGAGGTGCGGCCAGAGAACCAAGGGCCAGCTGCTGGCTGGAGAAGTCTACCTGCTC 12212

Qy 187 PheSerMetAlaLysIleProHisGluMetSerProAlaLeuHisArgLysIleSerVal 206
 Db 12213 TCAGATGGCCAGCTGCCACACGATGAGCCGGCCCTGCTGCACTGCG 12272

Qy 207 GluTyrGlyAspAlaPheHisProArgProHeCysMetArgArgValLysGluMetAsp 226
 Db 12273 CGTACCGTGAAGCCCTTCCACCCAGGCCCTCTGCTGATGCCAGGAGATGAC 12332

Qy 227 AlaTyrGlyMetValSerProHeAlaArgProSerValAsnSerAspLeuLysTyr 246
 Db 12333 GCCTATGGCAGTGTCTGCCCTGCCGCCAGGCTCACAGTCAGTC 12392

Qy 247 IleLysAlaLysValLeuArgGluLysGlnAlaArgGluLysAspLysCysThrIleGln 266
 Db 12393 ATCAGGCCAAGGCTCTGGGAAGGCCAGGCCGTTGAGGACAAGTGACCATCCAG 12452

RESULT 13
 US-10-723-060-458
 ; Sequence 458, Application US/10723860
 ; Publication No. US20040253606A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Aziz, Natasha
 ; APPLICANT: Ginsburg, Wendy M.
 ; APPLICANT: Zlonik, Albert
 ; TITLE OF INVENTION: Methods of Diagnosing of Soft Tissue Sarcoma, Compositions &

PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.1.1
SEQ ID NO 1
LENGTH: 846
TYPE: DNA
ORGANISM: Homo Sapien
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(843)
OTHER INFORMATION:
S-10-804-491-1